App Serial # 09/870,113   Exhibit B
Tumer et al.   LEX-0182-USA
Novel Human Mitochondrial Proteins and Polynucleotides Encoding the Same

>AJ303077 ACCESSION:AJ303077 NID: gi 12666719 emb AJ303077.1
          HSA303077 Homo sapiens mRNA for mitochondrial RNA
          splicing protein 3/4 (HMRS3/4 gene), 1448 bp cDNA splice
          variant
          Length = 1448

 Score = 760 bits (1940), Expect = 0.0
 Identities = 364/364 (100%), Positives = 364/364 (100%)
 Frame = +3

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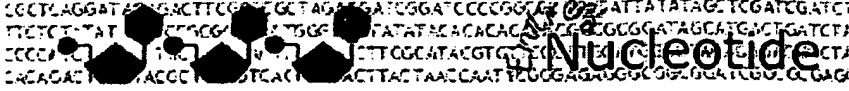
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☐ 1: AJ303077. Homo sapiens mRNA...[gi:12666719]   Links

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DEFINITION  Homo sapiens mRNA for mitochondrial RNA splicing protein 3/4
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ACCESSION   AJ303077
VERSION     AJ303077.1  GI:12666719
KEYWORDS    HMRS3/4 gene; mitochondrial RNA splicing protein 3/4.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Li,F.Y., Nikali,K., Gregan,J., Leibiger,I., Leibiger,B.,
            Schweyen,R., Larsson,C. and Suomalainen,A.
  TITLE     Characterization of a novel human putative mitochondrial
            transporter homologous to the yeast mitochondrial RNA splicing
            proteins 3 and 4
  JOURNAL   FEBS Lett. 494 (1-2), 79-84 (2001)                .
  MEDLINE   21195335
   PUBMED   11297739
REFERENCE   2  (bases 1 to 1448)
  AUTHORS   Nikali,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-DEC-2000) Nikali K., Human Molecular Genetics,
            National Public Health Institute, Mannerheimintie 166, Helsinki,
            FI-00300, FINLAND
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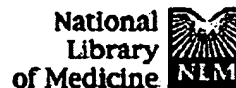
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//

Entrez-PubMed

App Serial # 09/870,113
Turner et al.
Novel Human Mitochondrial Proteins and Polynucleotides Encoding the Same

Exhibit C
LEX-0182-USA

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□ 1: FEBS Lett. 2001 Apr 6;494(1-2):79-84.   Related Articles, Links

ELSEVIER
FULL TEXT ARTICLE

Characterization of a novel human putative mitochondrial transporter homologous to the yeast mitochondrial RNA splicing proteins 3 and 4.

Li FY, Nikali K, Gregan J, Leibiger I, Leibiger B, Schweyen R, Larsson C, Suomalainen A.

Department of Molecular Medicine, CMM, Karolinska Hospital, Stockholm, Sweden. fangyuan.li@cmm.ki.se

We report here a novel human gene, hMRS3/4, encoding a putative mitochondrial transporter structurally and functionally homologous to the yeast mitochondrial RNA splicing proteins 3 and 4. These proteins belong to the family of mitochondrial carrier proteins (MCF) and are likely to function as solute carriers. hMRS3/4 spans approximately 10 kb of genomic DNA on chromosome 10q24 and consists of four exons that encode a 364-aa protein with six transmembrane domains. A putative splice variant, encoding a 177-aa protein with three transmembrane domains, was also identified. hMRS3/4 has a well-conserved signature sequence of MCF and is targeted into the mitochondria. When expressed in yeast, hMRS3/4 efficiently restores the mitochondrial functions in mrs3(o)mrs4(o) knock-out mutants. Ubiquitous expression in human tissues and a well-conserved structure and function suggest an important role for hMRS3/4 in human cells.

MeSH Terms:
- Alternative Splicing*
- Amino Acid Sequence
- Base Sequence
- Carrier Proteins/genetics*
- Carrier Proteins/metabolism
- Chromosome Mapping
- Chromosomes, Human, Pair 10*
- DNA, Complementary
- Fungal Proteins/genetics
- Gene Expression Profiling
- Human
- Membrane Transport Proteins*

- Mitochondria/metabolism*
- Molecular Sequence Data
- Mutagenesis
- Ophthalmoplegia, Chronic Progressive External/genetics
- RNA Splicing
- Repressor Proteins*
- Saccharomyces cerevisiae/genetics
- Saccharomyces cerevisiae Proteins*
- Spinocerebellar Ataxias/genetics
- Support, Non-U.S. Gov't
- Tissue Distribution
- Transfection

Substances:
- Carrier Proteins
- DNA, Complementary
- Fungal Proteins
- Membrane Transport Proteins
- Repressor Proteins
- SLC25A28 protein, human
- Saccharomyces cerevisiae Proteins
- MRS4 protein, S cerevisiae
- MRS3 protein, S cerevisiae
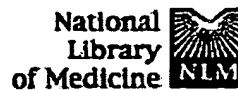
Secondary Source ID:
- GENBANK/AF327402
- GENBANK/AF327403
- GENBANK/AJ303077
- GENBANK/AJ303078

PMID: 11297739 [PubMed - indexed for MEDLINE]

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NCBI

National Library of Medicine **NLM**

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Display [Abstract ▼] Show: [20 ▼] [Sort ▼] Send to [Text ▼]

☐ 1: J Mol Biol. 1991 Jan 5;217(1):23-37.   Related Articles, Links

MRS3 and MRS4, two suppressors of mtRNA splicing defects in yeast, are new members of the mitochondrial carrier family.

Wiesenberger G, Link TA, von Ahsen U, Waldherr M, Schweyen RJ.

Institut fur Mikrobiologie und Genetik Universitat Wien, Austria.

When present in high copy number plasmids, the nuclear genes MRS3 and MRS4 from Saccharomyces cerevisiae can suppress the mitochondrial RNA splicing defects of several mit- intron mutations. Both genes code for closely related proteins of about Mr 32,000; they are 73% identical. Sequence comparisons indicate that MRS3 and MRS4 may be related to the family of mitochondrial carrier proteins. Support for this notion comes from a structural analysis of these proteins. Like the ADP/ATP carrier protein (AAC), the mitochondrial phosphate carrier protein (PiC) and the uncoupling protein (UCP), the two MRS proteins have a tripartite structure; each of the three repeats consists of two hydrophobic domains that are flanked by specific amino acid residues. The spacing of these specific residues is identical in all domains of all proteins of the family, whereas spacing between the hydrophobic domains is variable. Like the AAC protein, the MRS3 and MRS4 proteins are imported into mitochondria in vitro and without proteolytic cleavage of a presequence and they are located in the inner mitochondrial membrane. In vivo studies support this mitochondrial localization of the MRS proteins. Overexpression of the MRS3 and MRS4 proteins causes a temperature-dependent petite phenotype; this is consistent with a mitochondrial function of these proteins. Disruption of these genes affected neither mitochondrial functions nor cellular viability. Their products thus have no essential function for mitochondrial biogenesis or for whole yeast cells that could not be taken over by other gene products. The findings are discussed in relation to possible functions of the MRS proteins in mitochondrial solute translocation and RNA splicing.

PMID: 1703236 [PubMed - indexed for MEDLINE]

App Serial # 09/870,113   Exhibit E
Turner et al.   LEX-0182-USA
Novel Human Mitochondrial Proteins and Polynucleotides Encoding the Same

>BC047312 ACCESSION:BC047312 NID: gi 28703799 gb BC047312.1 Homo
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          clone IMAGE:5199184), partial cds
          Length = 1550

 Score = 760 bits (1940), Expect = 0.0
 Identities = 364/364 (100%), Positives = 364/364 (100%)
 Frame = +2

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□ 1: BC047312. Homo sapiens solu...[gi:28703799]   Links

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DEFINITION  Homo sapiens solute carrier family 25, member 28, mRNA (cDNA clone
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ACCESSION   BC047312
VERSION     BC047312.1  GI:28703799
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SOURCE      Homo sapiens (human)
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1550)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
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  TITLE     Generation and initial analysis of more than 15,000 full-length
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1550)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-FEB-2003) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
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Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
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Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 93 Row: i Column: 6.

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Jan 29 2004 15:38:25

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Query: 361 RAGK 364
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NCBI Nucleotide

| Entrez | PubMed | Nucleotide | Protein | Genome | Structure | PMC | Taxonomy | Books |

Search Nucleotide ▼ for [   ] [Go] [Clear]

Limits   Preview/Index   History   Clipboard   Details

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☐ **1: BC058937**. Homo sapiens solu...[gi:37747474]   Links

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ACCESSION   BC058937
VERSION     BC058937.1  GI:37747474
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
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  TITLE     Generation and initial analysis of more than 15,000 full-length
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1472)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-OCT-2003) National Institutes of Health, Mammalian
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            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Genome Sequence Centre,
            BC Cancer Agency, Vancouver, BC, Canada
```

info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 119 Row: k Column: 24.

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Jan 29 2004 15:38:25

App Serial # 09/870,113   Exhibit F
Turner et al.   LEX-0182-USA
Novel Human Mitochondrial Proteins and Polynucleotides Encoding the Same

characterize the protein. A starting material that can only be used to produce
a final product does not have a substantial asserted utility in those instances
where the final product is not supported by a specific and substantial utility. ·
In this case none of the proteins that are to be produced as final products
resulting from processes involving the claimed cDNA have asserted or
identified specific and substantial utilities. The research contemplated by
Applicants to characterize potential protein products, especially their
biological activities, does not constitute a specific and substantial utility.
Identifying and studying the properties of the protein itself or the
mechanisms in which the protein is involved does not define a "real world"
context of use. Note, because the claimed invention is not supported by a
specific and substantial asserted utility for the reasons set forth above,
credibility has not been assessed. Neither the specification as filed nor any
art of record discloses or suggests any property or activity for the cDNA
compounds such that another non-asserted utility would be well established
for the compounds.

Claim 1 is also rejected under 35 U.S.C. § 112, first paragraph.
Specifically, since the claimed invention is not supported by either a specific
and substantial asserted utility or a well established utility for the reasons set
forth above, one skilled in the art would not know how to use the claimed
invention.

Example 10: DNA Fragment encoding a Full Open Reading Frame (ORF)

Specification: The specification discloses that a cDNA library was prepared
from human kidney epithelial cells and 5000 members of this library were

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sequenced and open reading frames were identified. The specification discloses a Table that indicates that one member of the library having SEQ ID NO: 2 has a high level of homology to a DNA ligase. The specification teaches that this complete ORF (SEQ ID NO: 2) encodes SEQ ID NO: 3. An alignment of SEQ ID NO: 3 with known amino acid sequences of DNA ligases indicates that there is a high level of sequence conservation between the various known ligases. The overall level of sequence similarity between SEQ ID NO: 3 and the consensus sequence of the known DNA ligases that are presented in the specification reveals a similarity score of 95%. A search of the prior art confirms that SEQ ID NO: 2 has high homology to DNA Ligase encoding nucleic acids and that the next highest level of homology is to alpha-actin. However, the latter homology is only 50%. Based on the sequence homologies, the specification asserts that SEQ ID NO: 2 encodes a DNA ligase.

Claim 1: An isolated and purified nucleic acid comprising SEQ ID NO: 2.

Analysis: The following analysis includes the questions that need to be asked according to the guidelines and the answers to those questions based on the above facts:

1) Based on the record, is there a "well established utility" for the claimed invention? Based upon applicant's disclosure and the results of the PTO search, there is no reason to doubt the assertion that SEQ ID NO: 2 encodes a DNA ligase. Further, DNA ligases have a well-established use in the molecular biology art based on this class of protein's ability to ligate DNA. Consequently the answer to the question is yes.

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Note that if there is a well-established utility already associated with the claimed invention, the utility need not be asserted in the specification as filed. In order to determine whether the claimed invention has a well-established utility the examiner must determine that the invention has a specific, substantial and credible utility that would have been readily apparent to one of skill in the art. In this case SEQ ID NO: 2 was shown to encode a DNA ligase that the artisan would have recognized as having a specific, substantial and credible utility based on its enzymatic activity.

Thus, the conclusion reached from this analysis is that a 35 U.S.C. § 101 rejection and a 35 U.S.C. § 112, first paragraph, utility rejection should not be made.

Example 11: <u>Animals with Uncharacterized Human Genes</u>

Specification: Kidney cells from a patient with Polycystic Kidney (PCK) Disease have been used to make a cDNA library. From this library 8000 nucleotide "fragments" have been sequenced but not yet used to express proteins in a transformed host cell nor have they been characterized in any other way. The 50 longest fragments, SEQ ID NO: 1-50, respectively, have been used to make transgenic mice. None of the 50 lines of mice have developed Polycystic Kidney Disease to date. The asserted utility is the use of the mice to research human genes from diseased human kidneys. The disease is inheritable, but chromosomal loci have not yet been identified. Neither the absence or presence of a specific protein has been identified with the disease condition.

55

App Serial # 09/870,113   Exhibit G
Turner et al.   LEX-0182-USA
Novel Human Mitochondrial Proteins and Polynucleotides Encoding the Same

>AJ303077 ACCESSION:AJ303077 NID: gi 12666719 emb AJ303077.1
         HSA303077 Homo sapiens mRNA for mitochondrial RNA
         splicing protein 3/4 (HMRS3/4 gene), 1448 bp cDNA splice
         variant
         Length = 1448

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 Identities = 192/192 (100%), Positives = 192/192 (100%)
 Frame = +3

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Sbjct: 30   MELEGRGAGGVAGGPAAGPGRSPGESALLDGWLQRGVGRGAGGGEAGACRPPVRQDPDSG 209

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 Score = 405 bits (1030), Expect = e-111
 Identities = 192/192 (100%), Positives = 192/192 (100%)
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 Score = 405 bits (1030), Expect = e-111
 Identities = 192/192 (100%), Positives = 192/192 (100%)
 Frame = +3

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App Serial # 09/870,113   Exhibit H
Turner et al.   LEX-0182-USA
          Novel Human Mitochondrial Proteins and Polynucleotides Encoding the Same

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>AJ303077 ACCESSION:AJ303077 NID: gi 12666719 emb AJ303077.1
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          splicing protein 3/4 (HMRS3/4 gene), 1448 bp cDNA splice
          variant
          Length = 1448

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 Frame = +3

Query: 1   MELEGRGAGGVAGGPAAGPGRSPGESALLDGWLQRGVGRGAGGGEAGACRPPVRQDPDSG 60
            MELEGRGAGGVAGGPAAGPGRSPGESALLDGWLQRGVGRGAGGGEAGACRPPVRQDPDSG
Sbjct: 39   MELEGRGAGGVAGGPAAGPGRSPGESALLDGWLQRGVGRGAGGGEAGACRPPVRQDPDSG 218

Query: 61   PDYEALPAGATVTTHMVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWR 120
            PDYEALPAGATVTTHMVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWR
Sbjct: 219 PDYEALPAGATVTTHMVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWR 398

Query: 121 IIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVA 180
            IIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVA
Sbjct: 399 IIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVA 578

Query: 181 TLLHDAAMNPAE 192
            TLLHDAAMNPAE
Sbjct: 579 TLLHDAAMNPAE 614

App Serial # 09/870,113   Exhibit I
Turner et al.   LEX-0182-USA
Novel Human Mitochondrial Proteins and Polynucleotides Encoding the Same

```
>AJ303077 ACCESSION:AJ303077 NID: gi 12666719 emb AJ303077.1
          HSA303077 Homo sapiens mRNA for mitochondrial RNA
          splicing protein 3/4 (HMRS3/4 gene), 1448 bp cDNA splice
          variant
          Length = 1448

Identities = 93/93 (100%), Positives = 93/93 (100%), Gaps = 0/93 (0%)
 Frame = +3

Query: 1    MQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 60
            MQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL
Sbjct: 327  MQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 506

Query: 61   SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE 93
            SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE
Sbjct: 507  SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE 605




>BC047312 ACCESSION:BC047312 NID: gi 28703799 gb BC047312.1   Homo
          sapiens solute carrier family 25, member 28, mRNA (cDNA
          clone IMAGE:5199184), partial cds
          Length = 1550

 Identities = 93/93 (100%), Positives = 93/93 (100%), Gaps = 0/93 (0%)
 Frame = +2

Query: 1    MQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 60
            MQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL
Sbjct: 374  MQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 553

Query: 61   SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE 93
            SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE
Sbjct: 554  SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE 652




>BC058937 ACCESSION:BC058937 NID: gi 37747474 gb BC058937.1   Homo
          sapiens solute carrier family 25, member 28, mRNA (cDNA
          clone MGC:65184 IMAGE:6139015), complete cds
          Length = 1472

 Identities = 93/93 (100%), Positives = 93/93 (100%), Gaps = 0/93 (0%)
 Frame = +3

Query: 1    MQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 60
            MQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL
Sbjct: 336  MQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 515

Query: 61   SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE 93
            SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE
Sbjct: 516  SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE 614
```

App Serial # 09/870,113   Edition J
Turner et al.   LEX-0182-USA
Novel Human Mitochondrial Proteins and Polynucleotides Encoding the Same

Query= SEQ ID NO:1
            (1095 letters)

| | | Score | E |
| | | (bits) | Value |

Sequences producing significant alignments:

AL353719.10.1.123160   1031   0.0

>AL353719.10.1.123160
            Length = 123160

Identities = 520/520 (100%)
Strand = Plus / Minus

```
Query: 576    agtggtcaagcagaggatgcagatgtacaactcaccataccaccgggtgacagactgtgt 635
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 82990  agtggtcaagcagaggatgcagatgtacaactcaccataccaccgggtgacagactgtgt 82931


Query: 636    acgggcagtgtggcaaaatgaaggggccggggccttttaccgcagctacaccacccagct 695
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 82930  acgggcagtgtggcaaaatgaaggggccggggccttttaccgcagctacaccacccagct 82871


Query: 696    gaccatgaacgttcctttccaagccattcacttcatgacctatgaattcctgcaggagca 755
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 82870  gaccatgaacgttcctttccaagccattcacttcatgacctatgaattcctgcaggagca 82811


Query: 756    ctttaacccccagagacggtacaacccaagctcccacgtcctctctggagcttgcgcagg 815
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 82810  ctttaacccccagagacggtacaacccaagctcccacgtcctctctggagcttgcgcagg 82751


Query: 816    agctgtagctgccgcagccacaacccccactggacgtttgcaaaacactgctcaacaccca 875
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 82750  agctgtagctgccgcagccacaacccccactggacgtttgcaaaacactgctcaacaccca 82691


Query: 876    ggagtccttggctttgaactcacacattacaggacatatcacaggcatggctagtgcctt 935
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 82690  ggagtccttggctttgaactcacacattacaggacatatcacaggcatggctagtgcctt 82631


Query: 936    caggacggtatatcaagtaggtggggtgaccgcctatttccgaggggtgcaggccagagt 995
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 82630  caggacggtatatcaagtaggtggggtgaccgcctatttccgaggggtgcaggccagagt 82571


Query: 996    aatttaccagatcccctccacagccatcgcatggtctgtgtatgagttcttcaaatacct 1055
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 82570  aatttaccagatcccctccacagccatcgcatggtctgtgtatgagttcttcaaatacct 82511
```

```
Query: 1056   aatcactaaaaggcaagaagagtggagggctggcaagtga 1095
               ||||||||||||||||||||||||||||||||||||||||
Sbjct: 82510  aatcactaaaaggcaagaagagtggagggctggcaagtga 82471



Identities = 291/291 (100%)
Strand = Plus / Minus


Query: 1      atggagttggaggggcggggtgctggcggtgtggcggggggggccggcggcagggcccggg 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 91957  atggagttggaggggcggggtgctggcggtgtggcggggggggccggcggcagggcccggg 91898


Query: 61     cggagccccgggggagtcggcgctgctggacgggtggctgcagcggggcgtgggccgggggg 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 91897  cggagccccgggggagtcggcgctgctggacgggtggctgcagcggggcgtgggccgggggg 91838


Query: 121    gccggcggcggggaggccggggcctgcaggcccccggtacgacaagatccggactccggc 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 91837  gccggcggcggggaggccggggcctgcaggcccccggtacgacaagatccggactccggc 91778


Query: 181    ccggactacgaggcgctgccggctggagccactgtcaccacgcacatggtggcaggcgcc 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 91777  ccggactacgaggcgctgccggctggagccactgtcaccacgcacatggtggcaggcgcc 91718


Query: 241    gtggcagggatcctggagcactgcgtgatgtaccccatcgactgcgtcaag 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 91717  gtggcagggatcctggagcactgcgtgatgtaccccatcgactgcgtcaag 91667



Identities = 233/233 (100%)
Strand = Plus / Minus


Query: 290    agacccggatgcagagtctacagcctgacccagctgcccgctatcgcaatgtgttggagg 349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 85548  agacccggatgcagagtctacagcctgacccagctgcccgctatcgcaatgtgttggagg 85489


Query: 350    ccctctggaggattataagaacggagggcctatggaggcccatgaggggggctgaacgtca 409
              |||||||.||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 85488  ccctctggaggattataagaacggagggcctatggaggcccatgaggggggctgaacgtca 85429


Query: 410    cagcaacaggcgcagggcctgcccacgccctttattttgcctgctacgaaaagttaaaaa 469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 85428  cagcaacaggcgcagggcctgcccacgccctttattttgcctgctacgaaaagttaaaaa 85369
```

```
Query:   470    agacattgagtgatgtaatccaccctgggggcaatagccatattgccaatggt 522
                |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 85368    agacattgagtgatgtaatccaccctgggggcaatagccatattgccaatggt 85316



Identities = 58/58 (100%)
Strand = Plus / Minus


Query:   520    ggtgcggccgggtgtgtggcaacattacttcatgatgcagccatgaaccctgcggaag 577
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 84222    ggtgcggccgggtgtgtggcaacattacttcatgatgcagccatgaaccctgcggaag 84165
```

Query= SEQ ID NO:3
        (582 letters)

                                                         Score   E
Sequences producing significant alignments: (bits)   Value

AL353719.10.1.123160   577   e-162

>AL353719.10.1.123160
        Length = 123160

 Score = 577 bits (291), Expect = e-162
 Identities = 291/291 (100%)
 Strand = Plus / Minus

Query: 1   atggagttggagggggcggggtgctggcggtgtggcgggggggccggcggcagggcccggg 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 91957   atggagttggagggggcggggtgctggcggtgtggcgggggggccggcggcagggcccggg 91898

Query: 61   cggagccccgggggagtcggcgctgctggacgggtggctgcagcggggcgtgggccgggggg 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 91897   cggagccccgggggagtcggcgctgctggacgggtggctgcagcggggcgtgggccgggggg 91838

Query: 121   gccggcggcggggaggccggggcctgcaggcccccggtacgacaagatccggactccggc 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 91837   gccggcggcggggaggccggggcctgcaggcccccggtacgacaagatccggactccggc 91778

Query: 181   ccggactacgaggcgctgccggctggagccactgtcaccacgcacatggtggcaggcgcc 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 91777   ccggactacgaggcgctgccggctggagccactgtcaccacgcacatggtggcaggcgcc 91718

Query: 241   gtggcagggatcctggagcactgcgtgatgtaccccatcgactgcgtcaag 291
               |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 91717   gtggcagggatcctggagcactgcgtgatgtaccccatcgactgcgtcaag 91667

 Score = 462 bits (233), Expect = e-127
 Identities = 233/233 (100%)
 Strand = Plus / Minus

Query: 290   agacccggatgcagagtctacagcctgacccagctgcccgctatcgcaatgtgttggagg 349
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 85548   agacccggatgcagagtctacagcctgacccagctgcccgctatcgcaatgtgttggagg 85489

Query: 350   ccctctggaggattataagaacggagggcctatggaggcccatgaggggggctgaacgtca 409
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 85488   ccctctggaggattataagaacggagggcctatggaggcccatgaggggggctgaacgtca 85429

```
Query: 410    cagcaacaggcgcagggcctgcccacgcccctttattttgcctgctacgaaaagttaaaaa 469
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 85428  cagcaacaggcgcagggcctgcccacgcccctttattttgcctgctacgaaaagttaaaaa 85369


Query: 470    agacattgagtgatgtaatccaccctgggggcaatagccatattgccaatggt 522
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 85368  agacattgagtgatgtaatccaccctgggggcaatagccatattgccaatggt 85316



 Score =  117 bits (59), Expect = 8e-24
 Identities = 59/59 (100%)
 Strand = Plus / Minus


Query: 520    ggtgcggccgggtgtgtggcaacattacttcatgatgcagccatgaaccctgcggaagg 578
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct: 84222  ggtgcggccgggtgtgtggcaacattacttcatgatgcagccatgaaccctgcggaagg 84164
```

Sequences producing significant alignments:

Score E
(bits) Value

AL353719.10.1.123160

577 e-162

>AL353719.10.1.123160
       Length = 123160

 Score = 577 bits (291), Expect = e-162
 Identities = 291/291 (100%)
 Strand = Plus / Minus

Query: 1   atggagttggagggggcggggtgctggcggtgtggcggggggggccggcggcagggcccggg 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 91957 atggagttggagggggcggggtgctggcggtgtggcggggggggccggcggcagggcccggg 91898

Query: 61   cggagccccgggggagtcggcgctgctggacgggtggctgcagcggggcgtgggccggggg 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 91897 cggagccccgggggagtcggcgctgctggacgggtggctgcagcggggcgtgggccggggg 91838

Query: 121   gccggcggcggggaggccggggcctgcaggcccccggtacgacaagatccggactccggc 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 91837 gccggcggcggggaggccggggcctgcaggcccccggtacgacaagatccggactccggc 91778

Query: 181   ccggactacgaggcgctgccggctggagccactgtcaccacgcacatggtggcaggcgcc 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 91777 ccggactacgaggcgctgccggctggagccactgtcaccacgcacatggtggcaggcgcc 91718

Query: 241   gtggcagggatcctggagcactgcgtgatgtaccccatcgactgcgtcaag 291
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 91717 gtggcagggatcctggagcactgcgtgatgtaccccatcgactgcgtcaag 91667

 Score = 462 bits (233), Expect = e-127
 Identities = 233/233 (100%)
 Strand = Plus / Minus

Query: 290   agacccggatgcagagtctacagcctgacccagctgcccgctatcgcaatgtgttggagg 349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 85548 agacccggatgcagagtctacagcctgacccagctgcccgctatcgcaatgtgttggagg 85489

Query: 350   ccctctggaggattataagaacggagggcctatggaggcccatgaggggggctgaacgtca 409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 85488 ccctctggaggattataagaacggagggcctatggaggcccatgaggggggctgaacgtca 85429

```
Query:   410   cagcaacaggcgcagggcctgcccacgcccttattttgcctgctacgaaaagttaaaaa 469
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 85428   cagcaacaggcgcagggcctgcccacgcccttattttgcctgctacgaaaagttaaaaa 85369


Query:   470   agacattgagtgatgtaatccaccctgggggcaatagccatattgccaatggt 522
               |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 85368   agacattgagtgatgtaatccaccctgggggcaatagccatattgccaatggt 85316



  Score =  345 bits (174), Expect = 2e-92
  Identities = 174/174 (100%)
  Strand = Plus / Minus


Query:   520   ggtgcggccgggtgtgtggcaacattacttcatgatgcagccatgaaccctgcggaaggt 579
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 84222   ggtgcggccgggtgtgtggcaacattacttcatgatgcagccatgaaccctgcggaaggt 84163


Query:   580   aatgattcctcaacctatcactctgtgggcagctgcacctgtatttctttacagtttgca 639
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 84162   aatgattcctcaacctatcactctgtgggcagctgcacctgtatttctttacagtttgca 84103


Query:   640   gaagaaagcacatcagttttggtgggaaattctgttaccttgttttaccactag 693
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 84102   gaagaaagcacatcagttttggtgggaaattctgttaccttgttttaccactag 84049
```

        (396 letters)

<pre>
                                                              Score   E
Sequences producing significant alignments: (bits) Value

AL353719.10.1.123160   446   e-123
</pre>

>AL353719.10.1.123160
          Length = 123160

 Score = 446 bits (225), Expect = e-123
 Identities = 225/225 (100%)
 Strand = Plus / Minus

<pre>
Query: 1   atgcagagtctacagcctgacccagctgcccgctatcgcaatgtgttggaggccctctgg 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 85540   atgcagagtctacagcctgacccagctgcccgctatcgcaatgtgttggaggccctctgg 85481

Query: 61   aggattataagaacggagggcctatggaggcccatgaggggggctgaacgtcacagcaaca 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 85480   aggattataagaacggagggcctatggaggcccatgaggggggctgaacgtcacagcaaca 85421

Query: 121   ggcgcagggcctgcccacgccctttattttgcctgctacgaaaagttaaaaaagacattg 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 85420   ggcgcagggcctgcccacgccctttattttgcctgctacgaaaagttaaaaaagacattg 85361

Query: 181   agtgatgtaatccaccctggggggcaatagccatattgccaatggt 225
               |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 85360   agtgatgtaatccaccctggggggcaatagccatattgccaatggt 85316
</pre>

 Score = 345 bits (174), Expect = 1e-92
 Identities = 174/174 (100%)
 Strand = Plus / Minus

<pre>
Query: 223   ggtgcggccgggtgtgtggcaacattacttcatgatgcagccatgaaccctgcggaaggt 282
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 84222   ggtgcggccgggtgtgtggcaacattacttcatgatgcagccatgaaccctgcggaaggt 84163

Query: 283   aatgattcctcaacctatcactctgtgggcagctgcacctgtatttctttacagtttgca 342
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 84162   aatgattcctcaacctatcactctgtgggcagctgcacctgtatttctttacagtttgca 84103

Query: 343   gaagaaagcacatcagttttggtgggaaattctgttaccttgttttaccactag 396
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 84102   gaagaaagcacatcagttttggtgggaaattctgttaccttgttttaccactag 84049
</pre>
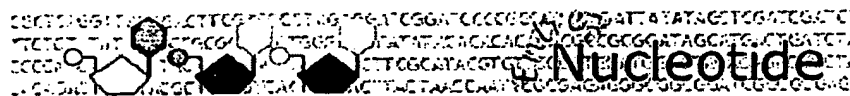
Entrez   PubMed   Nucleotide   Protein   Genome   Structure   PMC   Taxonomy   Books

Search | Nucleotide ▼ | for | _____ | | Go | | Clear |

Limits   Preview/Index   History   Clipboard   Details

Display | default ▼ | Show: | 20 ▼ | | Send to | | File ▼ | | Get Subsequence | | Featur|

☐ 1: <u>AL353719</u>. Human DNA sequenc...[gi:15787725]   Links

```
LOCUS       AL353719              123160 bp    DNA     linear   PRI 25-SEP-2001
DEFINITION  Human DNA sequence from clone RP11-85A1 on chromosome 10, complete
            sequence.
ACCESSION   AL353719 AC007643
VERSION     AL353719.10  GI:15787725
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 123160)
  AUTHORS   Ramsay,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
            requests: clonerequest@sanger.ac.uk
COMMENT     On Sep 26, 2001 this sequence version replaced gi:14280413.
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one plasmid subclone or more than one M13 subclone; and the
            assembly was confirmed by restriction digest. The following
            abbreviations are used to associate primary accession numbers given
            in the feature table with their source databases: Em:, EMBL; Sw:,
            SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
            database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
            was generated from part of bacterial clone contigs of human
            chromosome 10, constructed by the Sanger Centre Chromosome 10
            Mapping Group.  Further information can be found at
            http://www.sanger.ac.uk/HGP/Chr10
            RP11-85A1 is from the library RPCI-11.1 constructed by the group of
            Pieter de Jong. For further details see
            http://www.chori.org/bacpac/home.htm
            VECTOR: pBACe3.6
            IMPORTANT: This sequence is not the entire insert of clone
            RP11-85A1 It may be shorter because we sequence overlapping
            sections only once, except for a short overlap.
            The true left end of clone RP11-85A1 is at 1 in this sequence. The
            true left end of clone RP11-483F11 is at 123061 in this sequence.
```